



SEQUENCE LISTING

<110> NAGY et al.

<120> HUMAN POLYPEPTIDES CAUSING OR LEADING TO THE KILLING  
OF CELLS INCLUDING LYMPHOID TUMOR CELLS

<130> GPCG-P01-003

<140> 10/001934

<141> 2001-11-15

<150> PCT/US01/15625

<151> 2001-05-14

<160> 94

<170> PatentIn version 3.0

<210> 1

<211> 10

<212> PRT

<213> artificial sequence

<220>

<221> VHconCDR3

<222> (1)..(10)

<223> "Xaa" represents any amino acid residue

<400> 1

Xaa Xaa Xaa Xaa Arg Gly Xaa Phe Asp Xaa  
1 5 10

<210> 2

<211> 8

<212> PRT

<213> artificial sequence

<220>

<221> VLconCDR3

<222> (1)..(8)

<223> "Xaa" represents any amino acid residue

<400> 2

Gln Ser Tyr Asp Xaa Xaa Xaa Xaa  
1 5

<210> 3

<211> 8

<212> PRT

<213> artificial sequence

<220>

<221> Streptaq

RECEIVED

AUG 05 2003

TECH CENTER 1600/2900

<222> (1)..(8)

<400> 3

Trp Ser His Pro Gln Phe Glu Lys  
1 5

<210> 4

<211> 17

<212> DNA

<213> artificial sequence

<220>

<221> PrimerCRT5

<222> (1)..(17)

<400> 4

gtggtggttc cgatatc

17

<210> 5

<211> 44

<212> DNA

<213> artificial sequence

<220>

<221> PrimerCRT6

<222> (1)..(44)

<400> 5

agcgtcacac tcggtgcggc tttcggctgg ccaagaacgg gtta

44

<210> 6

<211> 10

<212> PRT

<213> artificial sequence

<220>

<221> MS-GPC1-VH-CDR3

<222> (1)..(10)

<400> 6

Gln Tyr Gly His Arg Gly Gly Phe Asp His  
1 5 10

<210> 7

<211> 13

<212> PRT

<213> artificial sequence

<220>

<221> MS-GPC1-VL-CDR1

<222> (1)..(13)

<400> 7

Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Tyr Val Ser  
1 5 10

<210> 8  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC1-VL-CDR3  
<222> (1)..(8)

<400> 8

Gln Ser Tyr Asp Phe Asn Glu Ser  
1 5

<210> 9  
<211> 9  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC6-VH-CDR3  
<222> (1)..(9)

<400> 9

Gly Tyr Gly Arg Tyr Ser Pro Asp Leu  
1 5

<210> 10  
<211> 12  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC6-VL-CDR1  
<222> (1)..(12)

<400> 10

Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala  
1 5 10

<210> 11  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC6-VL-CDR3  
<222> (1)..(8)

<400> 11

Gln Gln Tyr Ser Asn Leu Pro Phe  
1 5

<210> 12  
<211> 10  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-VH-CDR3  
<222> (1)..(10)

<400> 12

Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr  
1 5 10

<210> 13  
<211> 13  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-VL-CDR1  
<222> (1)..(13)

<400> 13  
Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Tyr Val Ser  
1 5 10

<210> 14  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-VL-CDR3  
<222> (1)..(8)

<400> 14

Gln Ser Tyr Asp Met Pro Gln Ala  
1 5

<210> 15  
<211> 10  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC10-VH-CDR3  
<222> (1)..(10)

<400> 15

Gln Leu His Tyr Arg Gly Gly Phe Asp Leu  
1 5 10

<210> 16  
<211> 13  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC10-VL-CDR1  
<222> (1)..(13)

<400> 16  
Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Tyr Val Ser  
1 5 10

<210> 17  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC10-VL-CDR3  
<222> (1)..(8)

<400> 17

Gln Ser Tyr Asp Leu Thr Met Gly  
1 5

<210> 18  
<211> 10  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-1-VH-CDR3  
<222> (1)..(10)

<400> 18  
Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr  
1 5 10

<210> 19  
<211> 13  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-1-VL-CDR1  
<222> (1)..(13)

<400> 19  
Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Tyr Val Ser  
1 5 10

<210> 20  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-1-VL-CDR3  
<222> (1)..(8)

<400> 20

Gln Ser Tyr Asp Phe Ser His Tyr  
1 5

<210> 21  
<211> 10  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-VH-CDR3  
<222> (1)..(10)

<400> 21

Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr  
1 10

<210> 22  
<211> 13  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-VL-CDR1  
<222> (1)..(13)

<400> 22  
Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Tyr Val Ser  
1 5 10

<210> 23  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-VL-CDR3  
<222> (1)..(8)

<400> 23

Gln Ser Tyr Asp Tyr Asp His Tyr  
1 5

<210> 24  
<211> 10  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-9-VH-CDR3  
<222> (1)..(10)

<400> 24  
Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr  
1 5 10

<210> 25  
<211> 13  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-9-VL-CDR1  
<222> (1)..(13)

<400> 25  
Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Tyr Val Ser  
1 5 10

<210> 26  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-9-VL-CDR3  
<222> (1)..(8)

<400> 26  
Gln Ser Tyr Asp Ile Gln Leu His  
1 5

<210> 27  
<211> 10  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-10-VH-CDR3  
<222> (1)..(10)

<400> 27  
Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr  
1 5 10

<210> 28  
<211> 13  
<212> PRT  
<213> artificial sequence  
  
<220>  
<221> MS-GPC8-10-VL-CDR1  
<222> (1)..(13)  
  
<400> 28  
Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Tyr Val Ser  
1 5 10

<210> 29  
<211> 8  
<212> PRT  
<213> artificial sequence  
  
<220>  
<221> MS-GPC8-10-VL-CDR3  
<222> (1)..(8)  
  
<400> 29  
Gln Ser Tyr Asp Leu Ile Arg His  
1 5

<210> 30  
<211> 10  
<212> PRT  
<213> artificial sequence  
  
<220>  
<221> MS-GPC8-17-VH-CDR3  
<222> (1)..(10)  
  
<400> 30  
Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr  
1 5 10

<210> 31  
<211> 13  
<212> PRT  
<213> artificial sequence  
  
<220>  
<221> MS-GPC8-17-VL-CDR1  
<222> (1)..(13)  
  
<400> 31  
Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Tyr Val Ser  
1 5 10

<210> 32  
<211> 8

<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-17-VL-CDR3  
<222> (1)..(8)

<400> 32

Gln Ser Tyr Asp Phe Ser Val Tyr  
1 5

<210> 33  
<211> 10  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-18-VH-CDR3  
<222> (1)..(10)

<400> 33  
Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr  
1 5 10

<210> 34  
<211> 13  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-18-VL-CDR1  
<222> (1)..(13)

<400> 34  
Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Tyr Val Ser  
1 5 10

<210> 35  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-18-VL-CDR3  
<222> (1)..(8)

<400> 35  
Gln Ser Tyr Asp Phe Ser Ile Tyr  
1 5

<210> 36  
<211> 10

<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-27-VH-CDR3  
<222> (1)..(10)

<400> 36  
Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr  
1 5 10

<210> 37  
<211> 13  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-27-VL-CDR1  
<222> (1)..(13)

<400> 37  
Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Tyr Val Ser  
1 5 10

<210> 38  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-27-VL-CDR3  
<222> (1)..(8)

<400> 38  
Gln Ser Tyr Asp Met Asn Val His  
1 5

<210> 39  
<211> 10  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-2-VH-CDR3  
<222> (1)..(10)

<400> 39  
Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr  
1 5 10

<210> 40  
<211> 13  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-2-VL-CDR1  
<222> (1)..(13)

<400> 40  
Ser Gly Ser Glu Ser Asn Ile Gly Ser Asn Tyr Val His  
1 5 10

<210> 41  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-2-VL-CDR3  
<222> (1)..(8)

<400> 41  
Gln Ser Tyr Asp Tyr Asp His Tyr  
1 5

<210> 42  
<211> 10  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-13-VH-CDR3  
<222> (1)..(10)

<400> 42  
Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr  
1 5 10

<210> 43  
<211> 13  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-13-VL-CDR1  
<222> (1)..(13)

<400> 43  
Ser Gly Ser Glu Ser Asn Ile Gly Ala Asn Tyr Val Thr  
1 5 10

<210> 44  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-13-VL-CDR3  
<222> (1)..(8)

<400> 44  
Gln Ser Tyr Asp Tyr Asp His Tyr  
1 5

<210> 45  
<211> 10  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-19-VH-CDR3  
<222> (1)..(10)

<400> 45  
Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr  
1 5 10

<210> 46  
<211> 13  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-19-VL-CDR1  
<222> (1)..(13)

<400> 46  
Ser Gly Ser Glu Ser Asn Ile Gly Ser Asn Tyr Val Ala  
1 5 10

<210> 47  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-19-VL-CDR3  
<222> (1)..(8)

<400> 47  
Gln Ser Tyr Asp Tyr Asp His Tyr  
1 5

<210> 48  
<211> 10  
<212> PRT  
<213> artificial sequence

<220>

<221> MS-GPC8-6-27-VH-CDR3  
<222> (1)..(10)

<400> 48  
Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr  
1 5 10

<210> 49  
<211> 13  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-27-VL-CDR1  
<222> (1)..(13)

<400> 49  
Ser Gly Ser Asp Ser Asn Ile Gly Ala Asn Tyr Val Thr  
1 5 10

<210> 50  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-27-VL-CDR3  
<222> (1)..(8)

<400> 50  
Gln Ser Tyr Asp Tyr Asp His Tyr  
1 5

<210> 51  
<211> 10  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-45-VH-CDR3  
<222> (1)..(10)

<400> 51  
Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr  
1 5 10

<210> 52  
<211> 13  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-45-VL-CDR1

<222> (1)..(13)

<400> 52  
Ser Gly Ser Glu Pro Asn Ile Gly Ser Asn Tyr Val Phe  
1 5 10

<210> 53  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-45-VL-CDR3  
<222> (1)..(8)

<400> 53  
Gln Ser Tyr Asp Tyr Asp His Tyr  
1 5

<210> 54  
<211> 10  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-47-VH-CDR3  
<222> (1)..(10)

<400> 54  
Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr  
1 5 10

<210> 55  
<211> 13  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-47-VL-CDR1  
<222> (1)..(13)

<400> 55  
Ser Gly Ser Glu Ser Asn Ile Gly Ser Asn Tyr Val Ser  
1 5 10

<210> 56  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-47-VL-CDR3  
<222> (1)..(8)

<400> 56

Gln Ser Tyr Asp Tyr Asp His Tyr  
1 5

<210> 57  
<211> 10  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-10-57-VH-CDR3  
<222> (1)..(10)

<400> 57  
Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr  
1 5 10

<210> 58  
<211> 13  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-10-57-VL-CDR1  
<222> (1)..(13)

<400> 58  
Ser Gly Ser Glu Ser Asn Ile Gly Asn Asn Tyr Val Gln  
1 5 10

<210> 59  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-10-57-VL-CDR3  
<222> (1)..(8)

<400> 59  
Gln Ser Tyr Asp Leu Ile Arg His  
1 5

<210> 60  
<211> 10  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-27-7-VH-CDR3  
<222> (1)..(10)

<400> 60  
Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr  
1 5 10

<210> 61  
<211> 13  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-27-7-VL-CDR1  
<222> (1)..(13)

<400> 61  
Ser Gly Ser Glu Ser Asn Ile Gly Asn Asn Tyr Val Gly  
1 5 10

<210> 62  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-27-7-VL-CDR3  
<222> (1)..(8)

<400> 62  
Gln Ser Tyr Asp Met Asn Val His  
1 5

<210> 63  
<211> 10  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-27-10-VH-CDR3  
<222> (1)..(10)

<400> 63  
Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr  
1 5 10

<210> 64  
<211> 13  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-27-10-VL-CDR1  
<222> (1)..(13)

<400> 64

Ser Gly Ser Glu Ser Asn Ile Gly Ala Asn Tyr Val Asn  
1 5 10

<210> 65  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-27-10-VL-CDR3  
<222> (1)..(8)

<400> 65  
Gln Ser Tyr Asp Met Asn Val His  
1 5

<210> 66  
<211> 10  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-27-41-VH-CDR3  
<222> (1)..(10)

<400> 66  
Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr  
1 5 10

<210> 67  
<211> 13  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-27-41-VL-CDR1  
<222> (1)..(13)

<400> 67  
Ser Gly Ser Glu Ser Asn Ile Gly Asn Asn Tyr Val Gln  
1 5 10

<210> 68  
<211> 8  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-27-41-VL-CDR3  
<222> (1)..(8)

<400> 68  
Gln Ser Tyr Asp Met Asn Val His  
1 5

<210> 69  
 <211> 3548  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <221> pMORPH13\_scFv  
 <222> (1)..(3548)  
  
 <400> 69

agagcatgcg	taggagaaaa	taaaaatgaaa	caaagcacta	ttgcactggc	actcttaccg	60
ttgctttca	cccctgttac	caaagccgac	tacaaagatg	aagtgcatt	ggttcagtct	120
ggcgcgaaag	tgaaaaaacc	gggcagcagc	gtgaaaagtga	gctgcaaagc	ctccggaggc	180
acttttagca	gctatgcgt	tagctgggt	cgccaagccc	ctgggcaggg	tctcgagtgg	240
atgggcccga	ttattccat	ttttggcactg	gcgaactacg	cgcagaagtt	tcagggccgg	300
gtgaccattt	ccgcggatga	aagcaccagc	accgcgtata	tggaactgag	cagcctgcgt	360
agcgaagata	cggccgtgta	ttattgcgcg	cgttattatg	atcgatgtt	taatatggat	420
tattggggcc	aaggcacccct	ggtgacggtt	agctcagcgg	gtggcggttc	tggcggcggt	480
gggagcggtg	gcggcggttc	tggcggtggt	ggttccgata	tcgaactgac	ccagccgcct	540
tcagtgagcg	ttgcaccagg	tcagaccgcg	cgtatctcg	gtagcggcga	tgcgtggc	600
gataaatacg	cgagctggta	ccagcagaaa	cccgggcagg	cgccagttct	ggtgatttat	660
gatgattctg	accgtccctc	aggcatcccg	gaacgcttta	gcggatccaa	cagcggcaac	720
accgcgaccc	tgaccattag	cggcaactcag	gcgaaagacg	aagcggatta	ttattgccag	780
agctatgacg	ctcatatgcg	tcctgtgtt	ggcggcggca	cgaagttaac	cgttcttggc	840
caggaattcg	agcagaagct	gatctctgag	gaggatctga	actagggtgg	tggctctgg	900
tccggtgatt	ttgattatga	aaagatggca	aacgctaata	agggggctat	gaccgaaaat	960
gccgatgaaa	acgcgctaca	gtctgacgct	aaaggcaaac	ttgattctgt	cgctactgtat	1020
tacggtgctg	ctatcgatgg	tttcatttgt	gacgtttccg	gccttgctaa	tggtaatgg	1080
gctactggtg	atttgctgg	ctctaattcc	caaatggctc	aagtcggtga	cggtgataat	1140
tcacctttaa	tgaataattt	ccgtcaatat	ttaccttccc	tccctcaatc	ggtgaatgt	1200
cgccttttg	tcttggcgc	tggtaaacca	tatgaatttt	ctattgattg	tgacaaaata	1260
aacttattcc	gtgggtgtctt	tgcgtttctt	ttatatgttg	ccacctttat	gtatgtattt	1320
tctacgtttg	ctaacataact	gcgtataataag	gagtcttgat	aagcttgacc	tgtgaagtga	1380
aaaatggcgc	agattgtgcg	acatttttt	tgtctggcgt	ttaatgaaat	tgtaaacgtt	1440

aatattttgt	taaaattcgc	gttaaatttt	tgtaaatca	gctcatttt	taaccaatag	1500
gccgaaatcg	gcaaaatccc	ttataaatca	aaagaataga	ccgagatagg	gtttagtgtt	1560
gttccagttt	ggaacaagag	tccactatta	aagaacgtgg	actccaacgt	caaagggcga	1620
aaaaccgtct	atcagggcga	tggcccacta	cgagaaccat	caccctaatac	aagtttttg	1680
gggtcgaggt	gccgtaaagc	actaaatcgg	aaccctaaag	ggagcccccg	atttagagct	1740
tgacgggaa	agccggcgaa	cgtggcgaga	aaggaaggga	agaaagcgaa	aggagcgggc	1800
gctagggcgc	tggcaagtgt	agcggtcacg	ctgcgcgtaa	ccaccacacc	cgccgcgcctt	1860
aatgcgccgc	tacagggcgc	gtgctagcca	tgtgagcaaa	aggccagcaa	aaggccagga	1920
accgtaaaaaa	ggccgcgttg	ctggcgtttt	tccataggct	ccgccccct	gacgagcatc	1980
acaaaaatcg	acgctcaagt	cagaggtggc	gaaacccgac	aggactataa	agataccagg	2040
cgtttcccc	tggaagctcc	ctcgtgcgt	ctcctgttcc	gaccctgccc	cttaccggat	2100
acctgtccgc	ctttctccct	tcgggaagcg	tggcgcttcc	tcatagctca	cgctgttaggt	2160
atctcagttc	ggttaggtc	gttcgctcca	agctggctg	tgtgcacgaa	ccccccgttc	2220
agtccgaccg	ctgcgcctta	tccggtaact	atcgcttga	gtccaacccg	gtaagacacg	2280
acttatcgcc	actggcagca	gccactggta	acaggattag	cagagcgagg	tatgtaggcg	2340
gtgctacaga	gttcttgaag	tggtggccta	actacggcta	cactagaaga	acagtatttg	2400
gtatctgcgc	tctgctgttag	ccagttacct	tcggaaaaag	agttggtagc	tcttgatccg	2460
gcaaacaaac	caccgctgg	agcgggtgg	ttttgtttt	caagcagcag	attacgcgc	2520
aaaaaaaagg	atctcaagaa	gatccttga	tctttctac	ggggtctgac	gctcagtgg	2580
acaaaaactc	acgttaaggg	atttggtca	gatctagcac	caggcggtt	agggcaccaa	2640
taactgcctt	aaaaaaatta	cgccccgccc	tgccactcat	cgcagtactg	ttgttaattca	2700
ttaagcattc	tgccgacatg	gaagccatca	caaacggcat	gatgaacctg	aatcgccagc	2760
ggcatcagca	ccttgcgc	ttgcgtataa	tattgccc	tagtggaaac	gggggcgaag	2820
aagttgtcca	tattggctac	gtttaaatca	aaactggta	aactcaccca	gggattggct	2880
gagacgaaaa	acatattctc	aataaaccct	ttagggaaat	aggccaggtt	ttcaccgtaa	2940
cacgcccacat	cttgcgaata	tatgtgtaga	aactgccgga	aatcgctgt	gtattcactc	3000
cagagcgatg	aaaacgtttc	agtttgcgtca	tggaaaacgg	tgtacaagg	gtgaacacta	3060
tcccatatca	ccagctcacc	gtcttcatt	gccatacgga	actccgggt	agcattcatc	3120
aggcgggcaa	gaatgtgaat	aaaggccgga	taaaacttgt	gcttattttt	cttacggtc	3180
tttaaaaagg	ccgtaatatac	cagctgaacg	gtctggttat	aggtacattg	agcaactgac	3240

tgaaatgcct caaaatgttc tttacgatgc cattggata tatcaacggt ggtatatacca 3300  
gtgattttt tctccatttt agcttcctta gctcctgaaa atctcgataa ctcaaaaaat 3360  
acgcccggta gtgatcttat ttcattatgg tgaaagttgg aacctcaccc gacgtcta 3420  
gtgagttagc tcactcatta ggcaccccaag gctttacact ttatgcttcc ggctcgat 3480  
ttgtgtggaa ttgtgagcgg ataacaattt cacacaggaa acagctatga ccatgattac 3540  
gaatttct 3548

<210> 70  
<211> 4410  
<212> DNA  
<213> artificial sequence

<220>  
<221> pMx7\_FS\_5D2  
<222> (1)..(4410)

<400> 70  
tctagagcat gcgttaggaga aaataaaatg aaacaaagca ctattgcact ggcactctta 60  
ccgttgctct tcacccctgt taccaaagcc gactacaaag atgaagtgca attggtgaa 120  
agcggcggcg gcctggtgca accgggcggc agcctgcgtc tgagctgcgc ggcctccgga 180  
tttacctta gcagctatgc gatgagctgg gtgcgccaag cccctggaa gggtctcgag 240  
tgggtgagcg cgattagcgg tagcggcggc agcacctatt atgcggatag cgtgaaaggc 300  
cgttttacca tttcacgtga taattcgaaa aacacccctgt atctgcaa 360  
atgcgttgc 360  
cgtgcggaaag atacggccgt gtattattgc ggcgtgtt 420  
agaagcattt ttctcgtaag  
aattggtttgc 480  
attattgggg ccaaggcacc ctggtgacgg ttagctcagc gggtggcggt 540  
tctggcggcg gtgggagcgg tggcggttgt tctggcggtg gtggttccga tatacgatg 600  
acccagagcc cactgagcct gccagtgact ccgggcgagc ctgcgagcat tagctgcaga 660  
agcagccaaa gcctgctgca tagcaacggc tataactatc tggattggta cttcaaaaaa 720  
ccaggtcaaa gcccgcagct attaatttat ctggcagca accgtgccag tgggtcccg 780  
gatcgttta gcggctctgg atccggcacc gattttaccc tgaaaattag ccgtgtggaa 840  
gctgaagacg tggcggtgtt 840  
ttattgcccag cagcattata ccaccccgcc gacctttggc  
cagggtacga aagttgaaat taaacgtacg gaattcgact ataaagatga cgatgacaaa 900  
ggcgccgcgt ggagccaccc gcagttgaa aaatgataag cttgacgtgt gaagtggaaa 960  
atggcgcaga ttgtgcgaca tttttttgt ctgcccgttta attaaagggg gggggggggcc 1020  
ggcctgggg ggggtgtaca tgaaaattgtt aacgttaata ttttgttaaa attcggtt 1080  
aattttgtt aaatcagctc attttttaac caataggccg aaatcgccaa aatcccttat 1140

aaatcaaaag aatagaccga gatagggttg agtgttgttc cagtttgaa caagagtcca	1200
ctattaaaga acgtggactc caacgtcaaa gggcgaaaaa ccgtctatca gggcgatggc	1260
ccactacgag aaccatcacc ctaatcaagt ttttgggt cgaggtgccg taaagcacta	1320
aatcggaacc ctaaagggag cccccgattt agagcttgac ggggaaagcc ggcgaacgtg	1380
gcgagaaagg aagggaaagaa a诶cgaaagga gcggcgcta gggcgctggc aagtgtagcg	1440
gtcacgctgc gcgttaaccac cacacccgcc gcgcttaatg cgccgctaca gggcgctgc	1500
tagacttagt tttaaaccgg accggggggg ggcttaagtg ggctgcaaaa caaaacggcc	1560
tccctgtcagg aagccgcttt tatcgggtag cctcaactgcc cgcttccag tcgggaaacc	1620
tgtcgtgcca gctgcatcag tgaatcgcc aacgcgcggg gagaggcggt ttgcgtattt	1680
ggagccaggg tggttttct tttcaccagt gagacggca acagctgatt gcccttcacc	1740
gcctggccct gagagagttt cagcaagcgg tccacgctgg tttgccccag cagggcaaaa	1800
tccctgttga tggtggtcag cggcggata taacatgagc tgtcctcggt atcgtcgat	1860
cccaactaccg agatgtccgc accaacgcgc agcccgact cggtaatggc acgcattgcg	1920
cccagcgcca tctgatcggt ggcaaccagc atcgcagtgg gaacgatgcc ctcattcagc	1980
atttgcattgg tttgttgaaa accggacatg gcactccagt cgcctcccg ttccgctatc	2040
ggctgaattt gattgcgagt gagatattta tgccagccag ccagacgcag acgcgcggag	2100
acagaactta atgggccagc taacagcgcg atttgcgtgt ggcccaatgc gaccagatgc	2160
tccacgcccc gtcgcgtacc gtcctcatgg gagaaaataa tactgttgat ggggtctgg	2220
tcagagacat caagaaataa cgccggaaca ttagtgcagg cagcttccac agcaatagca	2280
tcctggtcat ccagcggata gttaataatc agccactga cacgtgcgc gagaagattt	2340
tgcaccgcgg cttaacaggc ttgcacgcgg cttcgatctca ccatcgacac gaccacgctg	2400
gcacccagtt gatcggcgcg agatttaatc gcccgcacaa tttgcgacgg cgctgcagg	2460
gccagactgg aggtggcaac gccaatcagc aacgactgtt tgcccgccag ttgttgcgtt	2520
acgcggtagt gaatgtattt cagctccgcc atcgcgcattt ccacttttc ccgcgtttt	2580
gcagaaacgt ggctggcctg gttcaccacg cggaaacgg tctgataaga gacaccggca	2640
tactctgcga catcgatataa cgttactggt ttccacattca ccaccctgaa ttgactctct	2700
tccggcgct atcatgccat accgcgaaag gtttgcgtcc attcgatgtt agccatgtga	2760
gcaaaaggcc agcaaaaggc caggaaccgt aaaaaggccg cggtgcgtggc gttttccat	2820
aggctccgccc cccctgacga gcatcacaaa aatcgacgtt caagtcagag gtggcgaaac	2880
ccgacaggac tataaagata ccaggcggtt cccctggaa gctccctcggt gcgtctccct	2940

gttccgaccc	tgccgcttac	cggatacctg	tccgccttc	tcccttcggg	aagcgtggcg	3000
ctttctata	gctcacgctg	tagtatctc	agttcggtgt	aggtcgttcg	ctccaagctg	3060
ggctgtgtgc	acgaacccccc	cgttcagccc	gaccgctgctg	ccttataccgg	taactatcgt	3120
ctttagtcca	acccggtaag	acacgactta	tcgcccactgg	cagcagccac	tggtaacagg	3180
attagcagag	cgaggtatgt	aggcggtgct	acagagttct	tgaagtggtg	gcctaactac	3240
ggctacacta	gaagaacagt	atttggtatac	tgcgctctgc	tgtagccagt	tacttcggaa	3300
aaaagagttg	gtagcttttgc	atccggcaaa	caaaccaccg	ctggtagcgg	tggttttttt	3360
gtttgcaagc	agcagattac	gcmcagaaaa	aaaggatctc	aagaagatcc	tttgatcttt	3420
tctacgggtt	ctgacgctca	gtggaacgaa	aactcacgtt	aagggatttt	ggtcagatct	3480
agcaccaggc	gtttaaggc	accaataact	gccttaaaaaa	aattacgccc	cgccctgcca	3540
ctcatcgca	tactgttgc	attcattaag	cattctgccc	acatggaagc	catcacaaac	3600
ggcatgatga	acctgaatcg	ccagcggcat	cagcaccttg	tcgccttgcg	tataatattt	3660
gcccatagtg	aaaacggggg	cgaagaagtt	gtccatattt	gctacgttta	aatcaaaaact	3720
ggtgaaactc	acccagggat	tggctgagac	aaaaaacata	ttctcaataaa	accctttagg	3780
gaaataggcc	aggtttcac	cgtaacacgc	cacatcttgc	gaatataatgt	gtagaaactg	3840
ccggaaatcg	tcgtggatt	cactccagag	cgatgaaaac	gtttcagttt	gctcatggaa	3900
aacggtgtaa	caagggtgaa	cactatccca	tatcaccagc	tcaccgtctt	tcattgccc	3960
acggaactcc	gggtgagcat	tcatcaggcg	ggcaagaatg	tgaataaagg	ccggataaaaa	4020
cttgcgttta	tttttcttta	cggctttaa	aaaggccgta	atatccagct	gaacggtctg	4080
gttataggta	cattgagcaa	ctgactgaaa	tgcctcaaaa	tgttctttac	gatgccattt	4140
ggatatatca	acgggtgtat	atccagtat	tttttctcc	attttagctt	ccttagctcc	4200
tgaaaatctc	gataactcaa	aaaatacgcc	cggtagtgc	cttatttcat	tatggtaaaa	4260
gttggAACCT	cacccgacgt	ctaattgtgag	ttagctact	cattaggcac	cccaggcttt	4320
acactttatg	cttccggctc	gtatgttg	tggattgtg	agcggataac	aatttcacac	4380
aggaaacagc	tatgaccatg	attacgaatt				4410

<210> 71  
<211> 5020  
<212> DNA  
<213> artificial sequence

<220>  
<221> pMx9\_Fab\_GPC8  
<222> (1)..(5020)

<400> 71	
atcgtgctga cccagccgcc ttcagtgaat ggcgcaccag gtcagcgtgt gaccatctcg	60
tgttagcggca gcagcagcaa cattggcagc aactatgtga gctggtacca gcagttgccc	120
gggacggcgc cgaaactgct gatttatgt aacaaccagc gtccctcagg cgtgccggat	180
cgttttagcg gatccaaaag cgccaccagc gcgcgccttg cgattacggg cctgcaaagc	240
gaagacgaag cggattatta ttgccagagc tatgacatgc ctcaggctgt gttggcggc	300
ggcacgaagt ttaaccgttc ttggccagcc gaaagccgca ccgagtgtga cgctgttcc	360
gccgagcagc gaagaattgc aggcaacaa agcgcaccctg gtgtgcctga ttagcgactt	420
ttatccggga gccgtgacag tggcctggaa ggcagatgc agccccgtca aggcgggaggt	480
ggagaccacc acaccctcca aacaaagcaa caacaagtac gcggccagca gctatctgag	540
cctgacgcct gagcagtggaa agtcccacag aagctacagc tgccaggtca cgcatgaggg	600
gagcaccgtg gaaaaaaccg ttgcgccgac tgaggcctga taagcatgctg taggagaaaa	660
taaaatgaaa caaagcacta ttgcactggc actcttaccg ttgctcttca cccctgttac	720
caaagcccag gtgcaattga aagaaagcgg cccggccctg gtgaaaccga cccaaaccct	780
gaccctgacc tgtacctttt ccggatttag cctgtccacg tctggcgttg gcgtgggctg	840
gattcgccag ccgcctggga aagccctcga gtggctggct ctgattgattt gggatgtat	900
taagtattat agcaccagcc tgaaaaacgcg tctgaccatt agcaaagata cttcgaaaaaa	960
tcaggtggtg ctgactatga ccaacatggc cccgggtggat acggccacctt attattgcgc	1020
gcgttctcct cgttatcggt gtgctttga ttattggggc caaggcacccc tggtgacgg	1080
tagctcagcg tcgacccaaag gtccaagcgt gtcccgctg gctccgagca gcaaaagcac	1140
cagcggcggc acggctgccc tgggctgcct gttaaagat tattcccg aaccagtcac	1200
cgtgagctgg aacagcgggg cgctgaccag cggcgtgcattt acctttccgg cggtgctgca	1260
aagcagcggc ctgtatagcc tgagcagcgt tgtgaccgtg ccgagcagca gcttaggcac	1320
tcagacctat atttgcaccc tgaaccataa accgagcaac accaaagtgg ataaaaaaagt	1380
ggaaccgaaa agcgaattcg actataaaga tgacgatgac aaaggcgcgc cgtggagcca	1440
cccgcagttt gaaaaatgt aagcttgacc tgtgaagtga aaaatggcgc agattgtgcg	1500
acattttttt tgtctgccgt ttaattaaag gggggggggg gccggcctgg ggggggggtgt	1560
acatgaaattt gtaaacgtta atattttttt aaaaattcgat ttaaaattttt gttaaatcag	1620
ctcattttttt aaccaatagg ccgaaatcgcc caaaatccct tataaatcaa aagaatagac	1680
cgagataggg ttgagtggttgc ttccagtttgc gaacaagagt ccactattaa agaacgtgg	1740
ctccaaacgtc aaaggcggaa aaaccgtcta tcagggcgat ggcccactac gagaaccatc	1800

accctaatac	agttttttgg	ggtcgaggtg	ccgtaaagca	ctaaatcgga	accctaaagg	1860
gagcccccg	tttagagctt	gacggggaaa	gccggcgaac	gtggcgagaa	aggaagggaa	1920
gaaagcgaaa	ggagcggcg	ctagggcgt	ggcaagtgt	gcggtcacgc	tgcgctaac	1980
caccacaccc	gccgcgtta	atgcgccgt	acagggcg	tgctagacta	gtgtttaaac	2040
cggaccggg	gggggcttaa	gtgggctgca	aaacaaaacg	gcctcctgtc	aggaagccgc	2100
tttatcggg	tagcctca	gcccgc	cagtcggaa	acctgtcg	ccagctgcat	2160
cagtgaatcg	gccaacgcgc	ggggagaggc	ggttgcgt	ttgggagcca	gggtgg	2220
tctttcacc	agtgagacgg	gcaacagctg	attgccttc	accgcctggc	cctgagagag	2280
ttgcagcaag	cggccacgc	tggttgccc	cagcaggcga	aaatcctgtt	tgtgggtgt	2340
cagcggcggg	atataacatg	agctgtc	ggtatcg	tatcccacta	ccgagatgtc	2400
cgcaccaacg	cgcagcccg	actcgtaat	ggcacgcatt	gcccagcg	ccatctgatc	2460
gttggcaacc	agcatcg	tgggacgat	gccctcattc	agcatttgc	tggttgtt	2520
aaaaccggac	atggca	actcc	ccgttccgt	atcggctgaa	tttattgc	2580
agtgagat	ttatgcc	cagcc	agc	cagacgc	gagaca	2640
agctaacagc	gcgatttgc	ggtggccaa	tgcgaccaga	tgctccacgc	ccagtcgcgt	2700
accgtcctca	tgggagaaaa	taatacttt	gatgggtgt	tggcagaga	catcaagaaa	2760
taacgcccga	acattagtgc	aggcagcttc	cacagcaata	gcattcggt	catccagcgg	2820
atagttata	atcagcccac	tgacacgtt	cgcgagaaga	ttgtgcaccc	ccgtttaca	2880
ggcttcgacg	ccgcttcgtt	ctaccatcga	cacgaccacg	ctggcaccca	gttgatcg	2940
gcgagattt	atcgccgcga	caatttgcga	cggcgcgtgc	agggccagac	tggaggtggc	3000
aacgccaatc	agcaacgact	gtttgc	cagttgtgt	gccacgcgt	taggaatgt	3060
attcagctcc	gccatcgccg	cttccactt	ttcccggtt	ttcgcagaaa	cgtggctggc	3120
ctggttcacc	acgcgggaaa	cggctgtata	agagacaccc	gcatactctg	cgacatcgta	3180
taacgttact	ggttcacat	tcaccaccct	gaattgactc	tcttccggc	gctatcatgc	3240
cataccgcga	aagg	tttgc	gccattcgat	gctagccatg	tgagcaaaag	3300
ggccaggaac	cgtaaaaagg	ccgcgttgc	ggcg	tttgc	cataggctcc	3360
cgagcatcac	aaaaatcgac	gctcaagtca	gagg	ggcga	aacccgacag	3420
ataccaggcg	tttccct	gaagctcc	cgtgcgtct	cctgtccga	ccctgccc	3480
taccggatac	ctgtccgc	tttccct	ggaa	aggcgt	gctttctc	3540
ctgttaggtat	ctcagttcgg	tgttaggtcg	tgcgtccaa	ctggcgt	tgcacgaacc	3600

ccccgttcag cccgaccgct gcgccttatac cgtaactat cgtcttgagt ccaacccgg 3660  
aagacacgac ttatcgccac tggcagcagc cactggtaac aggattagca gagcgaggta 3720  
tgttaggcggt gctacagagt tcttgaagtgt gtggcctaactacggctaca ctagaagaac 3780  
agtatttggt atctgcgctc tgctgttagcc agttacacctc ggaaaaagag ttggtagctc 3840  
ttgatccggc aaacaaacca ccgctggtag cggtggtttt tttgtttgca agcagcagat 3900  
tacgcgcaga aaaaaaggat ctcaagaaga tccttgatc ttttctacgg ggtctgacgc 3960  
tcagtgaaac gaaaactcac gttaaggat tttggcaga tctagcacca ggcgttaag 4020  
ggcaccaata actgccttaa aaaaattacg cccgcctg ccactcatcg cagtaactgtt 4080  
gtaattcatt aagcattctg ccgacatgga agccatcaca aacggcatga tgaacctgaa 4140  
tcgcccagcgg catcagcacc ttgtcgccctt gcgtataata tttgcccata gtggaaacgg 4200  
gggcgaagaa gttgtccata ttggctacgt ttaaatcaaa actggtgaaa ctcacccagg 4260  
gattggctga gacgaaaaac atattctcaa taaacccttt agggaaatag gccaggtttt 4320  
caccgtaaca cgccacatct tgcgaatata tgtgtagaaa ctgcccggaaa tcgtcgtgg 4380  
attcactcca gagcgatgaa aacgtttcag tttgctcatg gaaaacggtg taacaagggt 4440  
gaacactatc ccatatcacc agctcaccgt ctccattgc catacgaaac tccgggtgag 4500  
cattcatcag gcgggcaaga atgtgaataa aggccggata aaacttgtc ttattttct 4560  
ttacggtctt taaaaaggcc gtaatatcca gctgaacggt ctggttatag gtacattgag 4620  
caactgactg aaatgcctca aaatgttctt tacgatgcca ttgggatata tcaacggtgg 4680  
tatatccagt gattttttc tccattttag ctcccttagc tcctgaaaat ctcgataact 4740  
caaaaaatac gcccggtagt gatcttattt cattatggtg aaagttggaa cctcacccga 4800  
cgtctaatgt gagttagctc actcattagg caccccgaggc tttacacttt atgcttccgg 4860  
ctcgatgtt gtgtgaaatt gtgagcggat aacaattca cacaggaaac agctatgacc 4920  
atgattacga atttcttagat aacgaggggca aaaaatgaaa aagacagcta tcgcgattgc 4980  
agtggactg gctggtttcg ctaccgtagc gcaggccgat 5020

<210> 72  
<211> 4145  
<212> DNA  
<213> artificial sequence

<220>  
<221> pMORPH18\_Fab\_GPC8  
<222> (1)..(4145)

<400> 72

tcagataacg agggcaaaaa atgaaaaaaga cagctatcgc gattgcagtg gcactggctg 60  
gttcgctac cgtagcgcag gccgatatcg tgctgaccca gccgccttca gtgagtggcg 120  
caccaggtaa gcgtgtgacc atctcgtgta gcggcagcag cagcaacatt ggcagcaact 180  
atgtgagctg gtaccagcag ttgcccggaa cggcgccgaa actgctgatt tatgataaca 240  
accagcgtcc ctcagggcgtg ccggatcggtt ttagcggatc caaaagcggc accagcgcga 300  
gccttgcgat tacgggcctg caaagcgaag acgaagcggaa ttattattgc cagagctatg 360  
acatgcctca ggctgtgttt ggcggcggca cgaagttaa ccgttcttgg ccagccgaaa 420  
gccgcaccga gtgtgacgct gttccgcgg agcagcgaag aattgcagggc gaacaaagcg 480  
accctgggtgc gcctgatttag cgactttat ccgggagccg tgacagtggc ctggaggca 540  
gatagcagcc ccgtcaaggc gggagtgagg accaccacac cctccaaaca aagcaacaac 600  
aagtacgcgg ccagcagcta tctgagcctg acgcctgagc agtggaaagtc ccacagaagc 660  
tacagctgcc aggtcacgca tgaggggagc accgtggaaa aaaccgttgc gccgactgag 720  
gcctgataag catgcgtagg agaaaataaa atgaaacaaa gcactattgc actggcactc 780  
ttaccgttgc tcttcacccc ttttacccaa gcccaggtgc aattgaaaga aagcggcccg 840  
gccctggtaa aaccgaccca aaccctgacc ctgacctgta cctttccgg atttagcctg 900  
tccacgtctg gcgttggcgt gggctggatt cgccagccgc ctgggaaagc cctcgagtg 960  
ctggctctga ttgattggga tgatgataag tattatagca ccagcctgaa aacgcgtctg 1020  
accattagca aagataacttc gaaaaatcag gtggtgctga ctatgaccaa catggacccg 1080  
gtggatacgg ccaccttata ttgcgcgcgt tctcctcggt atcgtggtgc ttttggatt 1140  
tggggccaag gcaccctggt gacggtagc tcagcgtcga ccaaaggccc aagcgtgttt 1200  
ccgctggctc cgagcagcaa aagcaccagc ggcggcacgg ctgcccctggg ctgcctgggtt 1260  
aaagattatt tcccggaaacc agtcaccgtg agctggaaaca gcggggcgt gaccagcggc 1320  
gtgcatacct ttccggcggt gctgcaaagc agcggcctgt atagcctgag cagcgttgc 1380  
accgtgccga gcagcagctt aggcaactcag acctatattt gcaacgtgaa ccataaaccg 1440  
agcaacacca aagtggataa aaaagtggaa ccgaaaagcg aattcgggggg agggagcggg 1500  
agcggtgatt ttgattatga aaagatggca aacgctaata agggggctat gaccgaaaat 1560  
gccgatgaaa acgcgtaca gtctgacgct aaaggcaac ttgattctgt cgctactgat 1620  
tacggtgctg ctatcgatgg tttcattggt gacggttccg gccttgcata tggtatgg 1680  
gctactggtg atttgctgg ctctaattcc caaatggctc aagtcggtaa cggtgataat 1740  
tcacctttaa tgaataattt ccgtcaatata ttaccttccc tccctcaatc ggtgaatgt 1800

cgccttttgc tcttggcgc tggtaaacca tatgaatttt ctattgattt tgacaaaata	1860
aacttattcc gtggtgtctt tgcgtttctt ttatatgttg ccacctttat gtatgtattt	1920
tctacgttttgc ctaacataact gcgtaataag gagtcttgc aagcttgcacc tgtgaagtga	1980
aaaatggcgc agattgtgcg acatttttt tgtctgccgt ttaatgaaat tgtaaacgtt	2040
aatattttgt taaaattcgc gttaaattttt tgttaaatca gtcattttt taaccaatag	2100
gccgaaatcg gcaaaatccc ttataaatca aaagaataga ccgagatagg gttgagtgtt	2160
gttccagttt ggaacaagag tccactatta aagaacgtgg actccaacgt caaagggcga	2220
aaaaccgtct atcagggcga tggcccacta cgagaaccat caccctaatac aagttttttg	2280
gggtcgaggt gccgtaaagc actaaatcg aaccctaaag ggagcccccg atttagagct	2340
tgacgggaa agccggcga cgtggcgaga aaggaaggaa agaaagcga aggagcggc	2400
gctagggcgc tggcaagtgt agcggtcacg ctgcgcgtaa ccaccacacc cgccgcgc	2460
aatgcgcgc tacagggcgc gtgctagcca tgtgagcaaa aggccagcaa aaggccagga	2520
accgtaaaaa ggccgcgttg ctggcgcccc tccataggct ccgccccct gacgagcatc	2580
acaaaaatcg acgctcaagt cagaggtggc gaaacccgac aggactataa agataccagg	2640
cgtttcccccc tggaagctcc ctcgtgcgtct ctcctgttcc gaccctgccc cttaccggat	2700
acctgtccgc ctttctccct tcgggaagcg tggcgcttcc tcatacgctca cgctgttaggt	2760
atctcagttc ggttaggtc gttcgctcca agctggctg tgtgcacgaa ccccccgttc	2820
agtccgaccg ctgcgcctta tccggtaact atcgtcttga gtccaaacccg gtaagacacg	2880
acttatcgcc actggcagca gccactggta acaggattag cagagcgagg tatgtaggcg	2940
gtgctacaga gttcttgaag tggtggcccta actacggcta cactagaaga acagtatttgc	3000
gtatctgcgc tctgctgttag ccagttaccc tcggaaaaag agttggtagc tcttgcgtcc	3060
gcaaaacaaac caccgctggt agcgggtggtt tttttgttttgc caagcagcag attacgcgc	3120
gaaaaaaaaagg atctcaagaa gatcctttga tctttctac ggggtctgac gctcagtggaa	3180
acgaaaaactc acgttaaggg attttggtca gatctgcac caggcggtta agggcaccaa	3240
taactgcctt aaaaaaatttgc cccccccccc tgccactcat cgcaactgttttgc ttgtattca	3300
ttaaggcattc tgccgacatg gaagccatca caaacggcat gatgaacctg aatcgccagc	3360
ggcatcagca ctttgcgtcc ttgcgtataa tatttgcgtccata tagtggaaac gggggcgaag	3420
aagttgtcca tattggctac gtttaaatca aaactggtga aactcacccaa gggattggct	3480
gagacgaaaa acatattctc aataaaccct ttagggaaat aggccaggtt ttcaccgtaa	3540
cacggccacat cttgcgaata tatgtgtaga aactgcccggaa aatcgtcggtt gtattcactc	3600

cagagcgatg aaaacgtttc agtttgctca tggaaaacgg tgtaacaagg gtgaacacta	3660
tcccatatca ccagctcacc gtcttcatt gccatacgga actccgggtg agcattcatc	3720
aggcgggcaa gaatgtgaat aaaggccgga taaaacttgt gcttattttt cttacggtc	3780
tttaaaaagg ccgtaataatc cagctgaacg gtctggttat aggtacattg agcaactgac	3840
tgaaatgcct caaaatgttc tttacgatgc cattggata tatcaacggt ggtatatcca	3900
gtgattttt tctccatttt agcttcctta gctcctgaaa atctcgataa ctcaaaaaat	3960
acgcccggta gtgatcttat ttcattatgg tgaaagttgg aacctcaccc gacgtctaat	4020
gtgagttagc tcactcatta ggcacccag gctttacact ttatgcttcc ggctcgtatg	4080
ttgtgtggaa ttgtgagcgg ataacaattt cacacaggaa acagctatga ccatgattac	4140
gaatt	4145

<210> 73  
 <211> 120  
 <212> PRT  
 <213> artificial sequence

<220>  
 <221> MS-GPC1-VH  
 <222> (1)..(120)

<400> 73

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln  
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser  
 20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu  
 35 40 45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser  
 50 55 60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val  
 65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr  
 85 90 95

Cys Ala Arg Gln Tyr Gly His Arg Gly Gly Phe Asp His Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
 115 120

<210> 74  
 <211> 109  
 <212> PRT

<213> artificial sequence

<220>

<221> MS-GPC1-VL

<222> (1)..(109)

<400> 74

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Asn Ile Gly Ser Asn  
20 25 30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu  
35 40 45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln  
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Asn Glu  
85 90 95

Ser Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105

<210> 75

<211> 118

<212> PRT

<213> artificial sequence

<220>

<221> MS-GPC6-VH

<222> (1)..(118)

<400> 75

Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Gly Tyr Gly Arg Tyr Ser Pro Asp Leu Trp Gly Gln Gly Thr

100

105

110

Leu Val Thr Val Ser Ser  
115

<210> 76  
<211> 110  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC6-VL  
<222> (1)..(110)

<400> 76

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ser Asn Leu Pro  
85 90 95

Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr  
100 105 110

<210> 77  
<211> 120  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-VH  
<222> (1)..(120)

<400> 77

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln  
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser  
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu  
35 40 45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser  
50 55 60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val  
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr  
85 90 95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 78

<211> 109

<212> PRT

<213> artificial sequence

<220>

<221> MS-GPC8-VL

<222> (1)..(109)

<400> 78

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn  
20 25 30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu  
35 40 45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln  
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Pro Gln  
85 90 95

Ala Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105

<210> 79

<211> 120

<212> PRT

<213> artificial sequence

<220>

<221> MS-GPC10-VH

<222> (1)..(120)

<400> 79

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln  
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser

20

25

30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu  
 35 40 45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser  
 50 55 60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val  
 65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr  
 85 90 95

Cys Ala Arg Gln Leu His Tyr Arg Gly Gly Phe Asp Leu Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
 115 120

<210> 80

<211> 109

<212> PRT

<213> artificial sequence

<220>

<221> MS-GPC10-VL

<222> (1)..(109)

<400> 80

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn  
 20 25 30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu  
 35 40 45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln  
 65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Leu Thr Met  
 85 90 95

Gly Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105

<210> 81

<211> 120

<212> PRT

<213> artificial sequence

<220>

<221> MS-GPC8-6-VH

<222> (1)..(120)

<400> 81

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln  
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser  
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu  
35 40 45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser  
50 55 60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val  
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr  
85 90 95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 82

<211> 109

<212> PRT

<213> artificial sequence

<220>

<221> MS-GPC8-6-VL

<222> (1)..(109)

<400> 82

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn  
20 25 30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu  
35 40 45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln  
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Asp His  
85 90 95

Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105

<210> 83  
<211> 120  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-10-VH  
<222> (1)..(121)

<400> 83

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln  
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser  
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu  
35 40 45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser  
50 55 60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val  
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr  
85 90 95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 84  
<211> 109  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-10-VL  
<222> (1)..(109)

<400> 84

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn  
20 25 30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu  
35 40 45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln  
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Leu Ile Arg  
85 90 95

His Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105

<210> 85  
<211> 120  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-17-VH  
<222> (1)..(120)

<400> 85  
Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln  
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser  
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu  
35 40 45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser  
50 55 60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val  
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr  
85 90 95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 86  
<211> 109  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-17-VL  
<222> (1)..(109)

<400> 86

Asp	Ile	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Gly	Ala	Pro	Gly	Gln
1						5			10					15	
Arg	Val	Thr	Ile	Ser	Cys	Ser	Gly	Ser	Ser	Ser	Asn	Ile	Gly	Ser	Asn
							20		25				30		
Tyr	Val	Ser	Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu
							35		40			45			
Ile	Tyr	Asp	Asn	Asn	Gln	Arg	Pro	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser
						50		55			60				
Gly	Ser	Lys	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile	Thr	Gly	Leu	Gln
						65		70			75		80		
Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Tyr	Asp	Phe	Ser	Val
						85			90			95			
Tyr	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly			
						100		105							

<210>	87															
<211>	120															
<212>	PRT															
<213>	artificial sequence															
<220>																
<221>	MS-GPC8-27-VH															
<222>	(1)..(120)															
<400>	87															
Gln	Val	Gln	Leu	Lys	Glu	Ser	Gly	Pro	Ala	Leu	Val	Lys	Pro	Thr	Gln	
1					5				10				15			
Thr	Leu	Thr	Leu	Thr	Cys	Thr	Phe	Ser	Gly	Phe	Ser	Leu	Ser	Thr	Ser	
					20			25			30					
Gly	Val	Gly	Val	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Ala	Leu	Glu	
						35		40			45					
Trp	Leu	Ala	Leu	Ile	Asp	Trp	Asp	Asp	Asp	Lys	Tyr	Tyr	Ser	Thr	Ser	
						50		55			60					
Leu	Lys	Thr	Arg	Leu	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	Asn	Gln	Val	
						65		70			75		80			
Val	Leu	Thr	Met	Thr	Asn	Met	Asp	Pro	Val	Asp	Thr	Ala	Thr	Tyr	Tyr	
						85			90			95				
Cys	Ala	Arg	Ser	Pro	Arg	Tyr	Arg	Gly	Ala	Phe	Asp	Tyr	Trp	Gly	Gln	
						100		105			110					
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser									
						115		120								

<210> 88

<211> 115  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-27-VL  
<222> (1)..(115)

<400> 88  
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15  
  
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn  
20 25 30  
  
Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu  
35 40 45  
  
Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60  
  
Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80  
  
Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Asn  
85 90 95  
  
Val His Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 110 115

<210> 89  
<211> 120  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-6-13-VH  
<222> (1)..(120)

<400> 89  
Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln  
1 5 10 15  
  
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser  
20 25 30  
  
Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu  
35 40 45  
  
Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser  
50 55 60  
  
Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val  
65 70 75 80  
  
Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr  
85 90 95  
  
Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln

	100	105	110
Gly Thr Leu Val Thr Val Ser Ser			
115	120		
<210> 90			
<211> 109			
<212> PRT			
<213> artificial sequence			
<220>			
<221> MS-GPC8-6-13-VL			
<222> (1)..(109)			
<400> 90			
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln			
1	5	10	15
Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Ser Asn Ile Gly Ala Asn			
20	25	30	
Tyr Val Thr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu			
35	40	45	
Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser			
50	55	60	
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln			
65	70	75	80
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Asp His			
85	90	95	
Tyr Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly			
100	105		

<210> 91			
<211> 120			
<212> PRT			
<213> artificial sequence			
<220>			
<221> MS-GPC8-10-57-VH			
<222> (1)..(120)			
<400> 91			
Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln			
1	5	10	15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser			
20	25	30	
Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu			
35	40	45	
Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser			
50	55	60	

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val  
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr  
85 90 95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 92  
<211> 109  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-10-57-VL  
<222> (1)..(109)

<400> 92  
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Ser Asn Ile Gly Asn Asn  
20 25 30

Tyr Val Gln Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu  
35 40 45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln  
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Leu Ile Arg  
85 90 95

His Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105

<210> 93  
<211> 120  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-27-41-VH  
<222> (1)..(120)

<400> 93  
Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln  
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser  
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu  
35 40 45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser  
50 55 60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val  
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr  
85 90 95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120

A  
) *contd*  
<210> 94  
<211> 109  
<212> PRT  
<213> artificial sequence

<220>  
<221> MS-GPC8-27-41-VL  
<222> (1)..(108)

<400> 94  
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Ser Asn Ile Gly Asn Asn  
20 25 30

Tyr Val Gln Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu  
35 40 45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln  
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Asn Val  
85 90 95

His Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105